OBSERVING THE CHANGE IN SOUTHEASTERN SPECIES' HABITAT AREAS DUE TO CLIMATE CHANGE

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OBSERVING THE CHANGE IN SOUTHEASTERN SPECIES'

HABITAT AREAS DUE TO CLIMATE CHANGE

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SUMMARY

The southeast United States is a critical place to study the effects of climate change on biodiversity because it contains the highest richness of plants and amphibians in the contiguous U.S. and has high levels of habitat fragmentation, limiting the abilities of these diverse fauna to track their habitats. We characterize the species distributions and species richness across the regions in current conditions and in the future under different climate scenarios. Our study examines ~300 vertebrate species that live in the southeastern U.S. including birds with limited dispersal abilities, mammals, reptiles, and amphibians. We identify the biodiversity hotspots today and in the future, investigate the current and future representation of species in protected areas in the Southeast, and identify potential areas of high conservation priority with respect to future range shifts due to climate change. We develop a methodological framework that starts with raw occurrence data from GBIF, uses careful subsampling approaches, Maxent distribution modeling based on climate covariates, and combines this with several ensembles of climate projections from the present to 2070. Within this framework, we extrapolate a consensus model given the suite of projected distributions. We identify which species will be most at risk of extinction, which will require movement connectivity to track their niches, and which will interact with urbanized areas.

CHAPTER 1

INTRODUCTION

Species have migrated in response to climate change in the past. However, current circumstances such as urbanization and the rapid speed of climate change resulting from greenhouse gas emissions pose new limitations as to where and how species can migrate [1]. Because of human presence in most of the world, current species will need to overcome obstacles that their ancestors did not. The statistics are startling: “less than 17% of the terrestrial landscape has escaped the direct impact of human activities, approximately half of the land surface has been converted to, and less than 1% of the world’s rivers remain unaffected by humans” [1]. Not only do modern species need to navigate developed areas, but also many species may not be able to migrate fast enough to keep up with their rapidly changing climate. On average, 9.2% of mammals will not be able to migrate at the pace of their climate due to their dispersal distance, and “87% of mammalian species are expected to experience reductions in range size and 20% of these range reductions will likely be due to limited dispersal abilities as opposed to reductions in the area of suitable climate” [2]. In particular, the southeastern region of the USA has been identified as a region “with projected high density of climate-driven movement,” as well as a highly urbanized region [1], which is why we chose this region for our project. Although analysis has been done of the southeast, there has been no overall study focused on the Southeast that includes all terrestrial species. Research in this area would help us determine what decisions can be made for the greater good of most species in the southeast.

The focus of this project is to determine how climate change and human development in the Southeast will affect ~300 terrestrial species' habitat and their ability to migrate. Using datasets of species presence records and modern climate data, we can estimate species distribution models to find each species' habitat niche and the locations of suitable habitat. Applying these models to projections of future climates, we can predict how the species suitable habitat will change over time. Once complete, these distribution maps will show the habitat suitability from 2010-2070 based on four different climate scenarios: Representative Concentration Pathways (RCP) 2.6, 4.5, 6.0, and 8.5. One of our objectives is to use the current and projected species distributions to estimate the expansion and shrinkage of species habitat over time, as well as the spatio-temporal changes in overall biodiversity. We will also estimate the percentage of habitat in protected areas [3] and in urbanized areas [4], as well as the distance that we expect the species' climatic niche to shift [5, 6]. This will help us identify individual or group of species that are particularly vulnerable. Using all four RCPs will show us how species will be affected not only by climate change and urbanization in general, but also by humans' rate of greenhouse gas production. This data might potentially demonstrate that if we can reduce greenhouse gas emissions, we can dramatically affect a species' chance of survival, which is a powerful motivational tool to convince people to be environmentally conscious. The second main objective is to calculate the migration corridors that each species must travel every decade in order to keep up with the changing climate, while taking into account the species-specific dispersal distance limits (following [7]). Analyzing the migration corridors for a large number of species will help us identify geographical areas in the Southeast that are critical to a large number of

species' ability to survive their new obstacles. Our results will help inform policy-makers how to prioritize conservation efforts in the southeastern USA, which is the ultimate goal of our project.

CHAPTER 2

LITERATURE REVIEW

In our project, we plan to create species distribution models for about 300 species in the southeastern US that show each species' climatic niche, and then project these models onto a variety of climates to see how each species will be affected by climate change. There are multiple steps to this project, including finding accurate climate data to use for training and projections, creating distribution models that account for as many biases as possible, and finding the trends in an overwhelming number of species. Luckily, there exists prior research in most steps of our project so that we can either reproduce certain methods or make modifications that suit our own study. Species distribution modeling is a relatively new area of interest in ecology and climate change research, and these models are being used for a variety of purposes. Some research papers focus on comparing the habitat range of different species in order to make conclusions about the relationships between these species [8], or they attempt to alleviate the negative effects of immediate landscape change on specific endangered species where there is a lack of data [9]. However, because in our study we are using our species distribution models to project onto future climate data, we will be mostly focusing on literature that either discusses methods to make species distribution models as accurate as possible, or those that involve future projected climate models.

There are many species distribution modelling algorithms available, but we are using one called Maxent, or "maximum entropy modeling" [10] because it is one of the highest performing algorithms [11] and in general does not require many modifications

other than the default algorithm settings. While in many studies, the Maxent algorithm is used as-is, there are other data preprocessing techniques to alleviate sampling bias in the species occurrence locations, the location of species' absences (if we know where a species is located, where can we infer that they are not?), and how to limit autocorrelation in the environmental data layers. There were two different papers published in 2014 that propose similar methods to alleviate sampling bias in species occurrence locations using environmental filtering instead of the old standard of geographic filtering [12, 13]. Sampling bias can occur in species occurrence location points because when researchers are searching for a specific species, they have a much higher chance of searching for these species near roads, civilization, or conservation units. Both studies' results indicated that using environmental filtering instead of geographic filtering or no filtering resulted in more accurate model predictions. However, de Oliveira's study [13] used actual species presence data to train the study while Varela's study [12] used a virtually created species with an artificially created sampling bias. While we preferred de Oliveira's study because of its evaluation of real species data, both these studies came to the same conclusion. Therefore we plan to use environmental filtering in our study. There have been multiple papers published on where to select pseudo-absences from species presence points [14, 15], but none of these papers address absences in Maxent because it is considered to be primarily a 'presence-only' algorithm. However, the Maxent software artificially creates its own variation of pseudo-absences called background points, so Maxent is not truly a presence-only software [10, 16]. Maxent chooses its background points randomly from the background area of inputted environmental data layers in order to decrease computation time, but we believe that it is possible to make this process more

accurate by creating buffered ranges around the occurrence points and selecting background points from within this range.

We are not the first people to use Maxent with future climate projections. However, we are the first to use future climate projections with such a large number of species within the southeast US. Another study which uses a large number of species is one by J. J. Lawler in 2013 that observes "Projected climate-driven faunal movement routes" [1]. The purpose of Lawler's study was to observe the distributions of 2903 vertebrate species in the western hemisphere, and the extent to which the species that need to migrate because of climate change, will be obstructed by "human-dominated landscapes" [1]. Lawler succeeded in finding key areas of concern; the southeastern United States was an area identified with "both projected high densities of climate-driven movements" as well as an area "heavily impacted by human activities" [1] and therefore is an area of concern. While Lawler's study identifies these areas of concern, it does not propose what can be done within the areas to aid with conservation planning and to preserve as many species as possible. According to Lawler, "there is ample opportunity for analytical innovations that could lead to more fine-grained analyses in the future." [1] This is why our study focuses on the southeast and looks at a much smaller scale to see locations that will benefit many southeastern species in their migrations.

Once we have our projected species distribution models, we plan to calculate the migration corridors for each species to identify the migration paths, as affected by both climate change and urbanization. A study by Steven J. Phillips in 2008 calculates the dispersal corridors for the Cape Proteaceae, a family of endemic plants [7]. This paper provides a method that will be useful to us in calculating our migration corridors using

network flow [7]. Much like our study is focused on the southeast US, this study is focused on the geographic location of the Western Cape of South Africa. However, Phillips's study was investigating a specific family of plants, while we are applying similar methods to multiple species of terrestrial animals. The goal in Phillips's methods was to find the "smallest possible newly protected area" using the dispersal corridors in order to more efficiently prioritize conservation efforts for this species. This application of computer science and mathematical principles to the ecology field is one of the main reason we are attracted to this topic, and Phillip's paper is a great example of an application these principles. However, the methods will have to be modified for our geographic location and different types of species.

A major factor in calculating the migration corridors is the dispersal distance for each species. If we do not take into account a reasonable distance that each species can be expected to migrate every decade, we could be predicting migration corridors that are impossible for the species. This is important to take into consideration because it has been indicated as an area of concern for mammals [2]. This study also used a relatively large number of species in their observations, with a total of 493 mammals in the Western Hemisphere and their dispersal distances to observe if the species will be able to keep up with their rapidly changing climates. Logistically, it is difficult to find the reasonable dispersal distance for each species, so it is helpful to see this study's approach to the issue. In calculated the dispersal distances, the study assumed that "successful reproduction occurs at the youngest age biologically possible and that the offspring in each generally survive to dispersal age and successfully disperse" when "in reality, dispersal has high associated mortality" [2]. Another study that required the dispersal

distances of their species by providing surveys to “experts” and asking them to estimate the dispersal distance, which we feel is both impossible, given our number of species, and prone to human error [17]. Regardless of the method we will eventually use in finding these dispersal distances, we know that they are important to consider on our migration corridors.

Although many studies have been done in this field, few exist that perform a collective examination that considers all terrestrial species in a geographic area and their projected habitats. We hope that our study will be able to provide detailed insight into what actions can be taken in the southeast US to assist in the survival of as many species as possible, with an emphasis on protecting already endangered species. These results can be used to inform policy makers where to prioritize their conservation efforts. In order to make these results as accurate as possible, it is important for us to consider the papers which detail useful methods. These methods can enhance both the species distribution modeling algorithms and processing the results in intuitive ways.

CHAPTER 3

MATERIALS AND METHODS

3.1 Data

Our collection of species to study was obtained from the Southeast Gap Analysis Project [18]. We obtained our occurrence locations for each of these species from the Global Biodiversity Information Facility (GBIF) [19] library. The GBIF database holds records of where and when species samples were collected. We obtained environmental data layers to train our species occurrence models from WorldClim [20], and the models were projected on different climate data to get future species' habitat predictions for 2030, 2050, and 2070 [21]. All together, we have thirteen habitat suitability data layers: one for the modern data/2010, and 4 for each year 2030, 2050, and 2070 for each RCP emissions scenario. Each species in our list will have its own Maxent species distribution model and 13 habitat suitability data layers. We found protected area data from the United States Geological Survey (USGS) [3] and projected urbanized data from 2010-2100 [4]. Data that shows the land cover type for all of the USA can be found at the Multi-Resolution Characteristic Consortium (MRLC)'s National Land Cover Database (NLCD). Water data layers were used to create a distance to water raster [22] to help train the models, and remove bodies of water from our maps so that habitats were not predicted to be in water.

3.2 Methods

We use the occurrence locations as presence points for each species, and remove all duplicates from the dataset. While Maxent provides the option to automatically select background points, this process is computationally expensive for multiple repetitions as

the raster data of the background points must be extracted for each run. Therefore, we used a different method for selecting background points. First, we created a convex hull around the occurrence points using a tool in the SDM Toolbox. The convex hull was 200 km way from the points. These convex hull polygons were used as a mask against the modern environmental rasters. Using a Maxent tool, we extracted 100,000 points from these clipped rasters. The 100,000 points were randomly partitioned into 100 different background point files. Our number of background points for each run in the experiments was 10,000, the same number used by Maxent.

The occurrence points are then environmentally subsampled using the methodology in Varela's paper [12]. Environmental subsampling of the data has been shown to improve model accuracy by removing points that are too similar according to the environmental data. The alternative method of sampling is geographic sampling, which removes points that are physically too close together. Varela's paper showed that environmentally subsampling data is more effective. We created 100 different versions of the subsampling data. Varela's method initially just chose the first point in each category, but we randomized each set of points by choosing a random point in the category where many occurrences were considered too environmentally similar.

These presence points and the current environmental data are loaded into Maxent species distribution software [10] to generate the species distribution models. These models are then projected onto the different future climatic data. After creating binary presence/absence maps that show where a species could survive [6, 9, 23-25], we can continue with our processing at another time. We also found the percentage of the distributions that are in a protected area [3] or an urbanized area [4]. To observe the range

shifts, we found the change in centroid of the suitable areas and created a map that shows the location of each species during each time period [5, 6].

The most important visualization that we have done with this data is creating maps that show the location of species over the four decades using a color-coded binary encoding. Because of the four time periods, there were sixteen binary encodings corresponding to either 1: present in this time period, or 0: not present in this time period (eg. 0000 means the species was never present in this pixel, 1000 means the species is only in this pixel in 2010). These maps allow us to view the habitat range shifts.

3.3 Future Methods

The *resistance to movement* layers that we need to find the movement corridors must be created for each species. The easiest design for these resistance layers is the inverse of the habitat suitability distribution data, but we plan to make resistance layers that account for land cover type. This way, we can assign a resistance value to different land cover types, such as urbanized areas [4], water [22], elevated regions, etc. Each species also has a dispersal distance that is a distance reasonable for the species to migrate to in a given year in order to stay with its climatic niche [2]. This will have to be collected for each species and can be used in the resistance layers. We will use the resistance layers to find the migration corridors for each species over the years 2010-2070. Because we are using a collection of 300 species, when we assemble all of the corridors we will be able to identify geographic regions with a high anticipated amount of migration. We can infer that these areas are high priority for conservation, because if they are urbanized or developed, many species may not be able to migrate to a climate where they can survive.

This project has been done primarily though programming using the language R [26]. Many of the R scripts use R-packages, including rgbif [27], raster [28], biomod2 [29], parallel, and graphics. These packages can be used for visualization of both plots and the maps, but we are also using ArcGIS Desktop [30] to visualize the species distribution maps and the species occurrence points. All scripts are available for public use and are available for download at https://github.gatech.edu/rbach3/SDM_Project. Because much of this project was in developing our methodology and automating the process using R scripts, time was devoted to creating an R package for easier use in the future.

CHAPTER 4

RESULTS

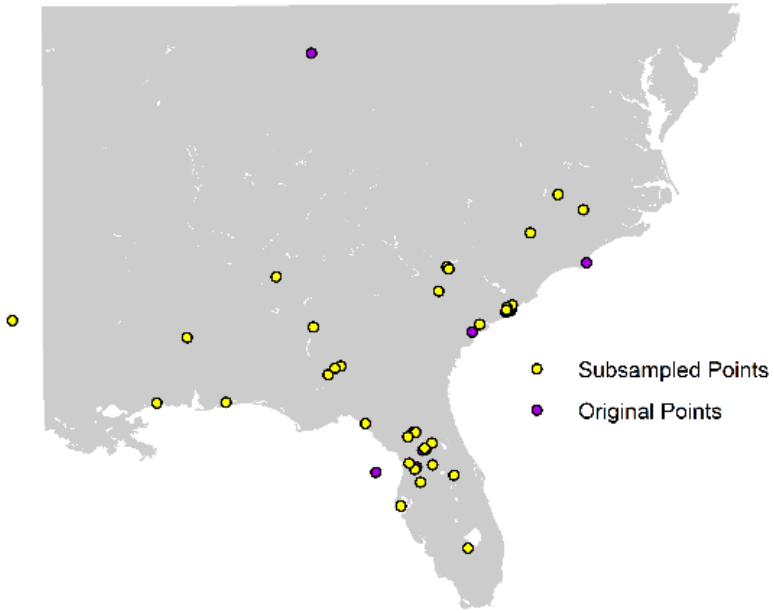
We were able to obtain results for forty seven species. The distribution of these species is as follows:

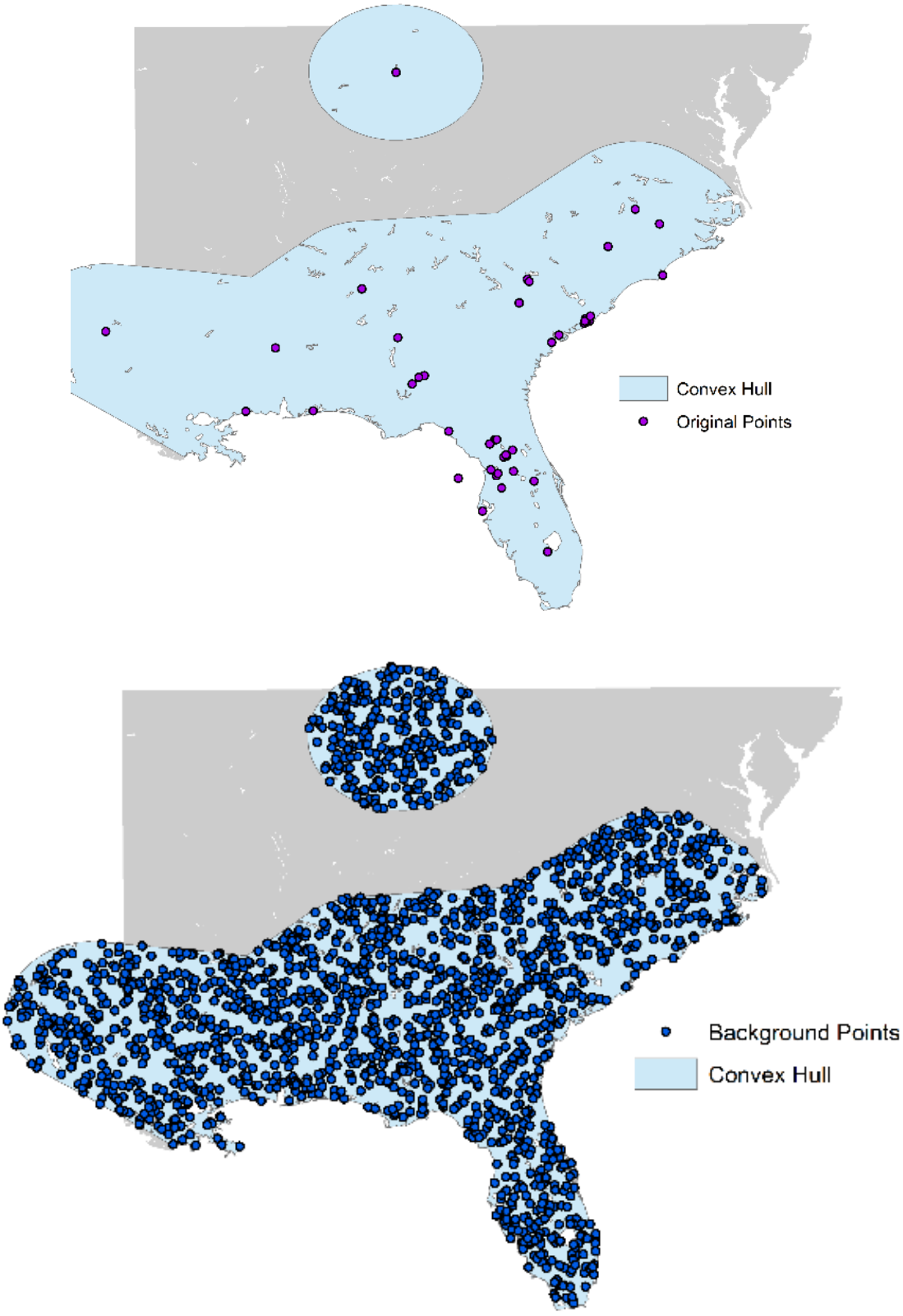
Total Species	# > 80% in SE	# Mammals	# Reptiles	# Amphibians
47	44	6	12	28

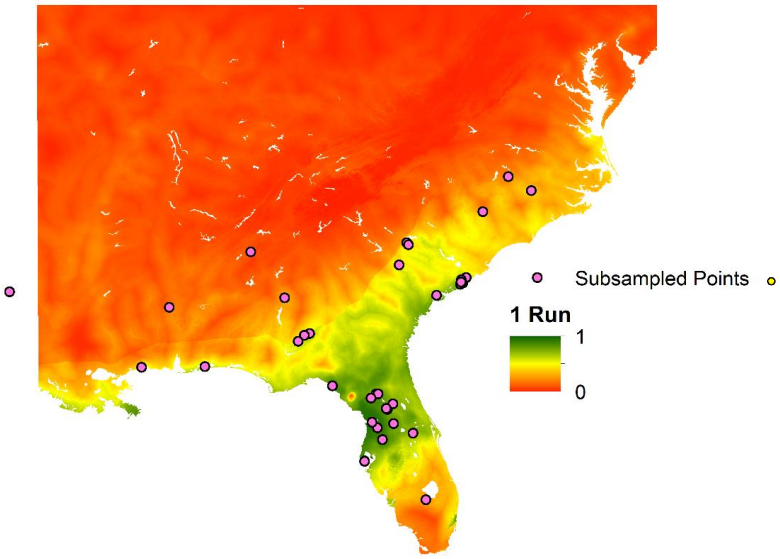
Although we were not able to obtain results for every species, we prioritized those with the highest percentage of occurrences in the southeast, as this region was the focus of our study.

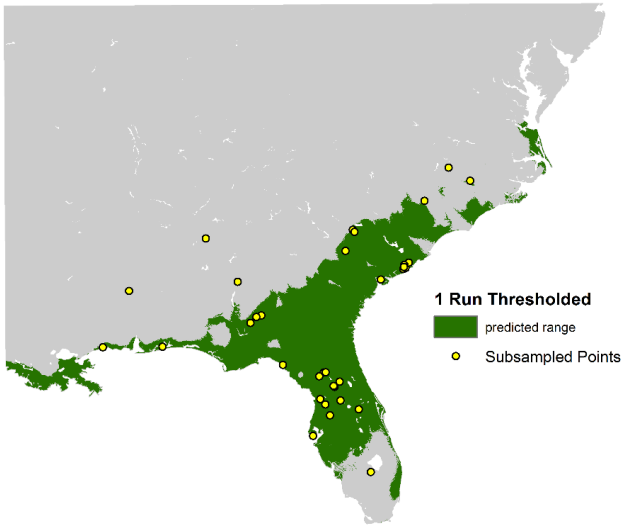
4.1 Species Specific Results

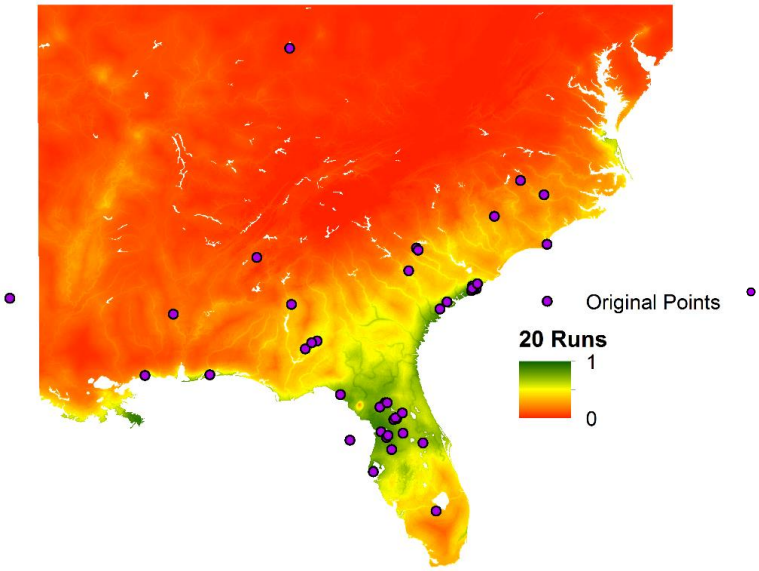
One of our species, the *Heterodon simus*, will be used as an example to demonstrate the results we have for every species.

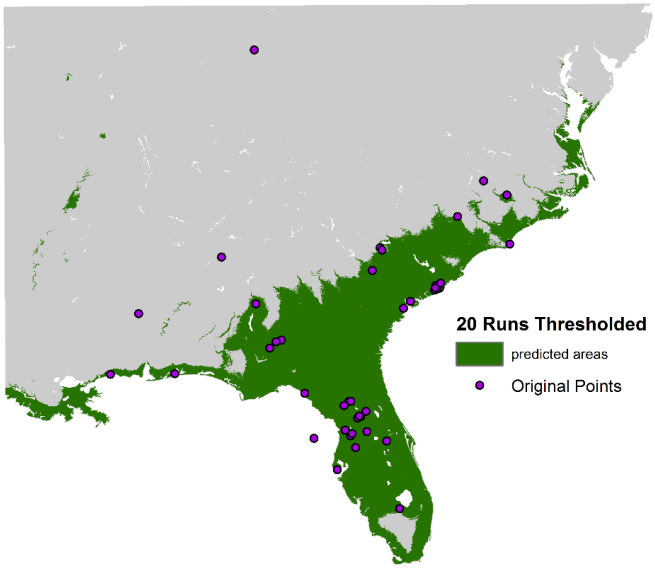


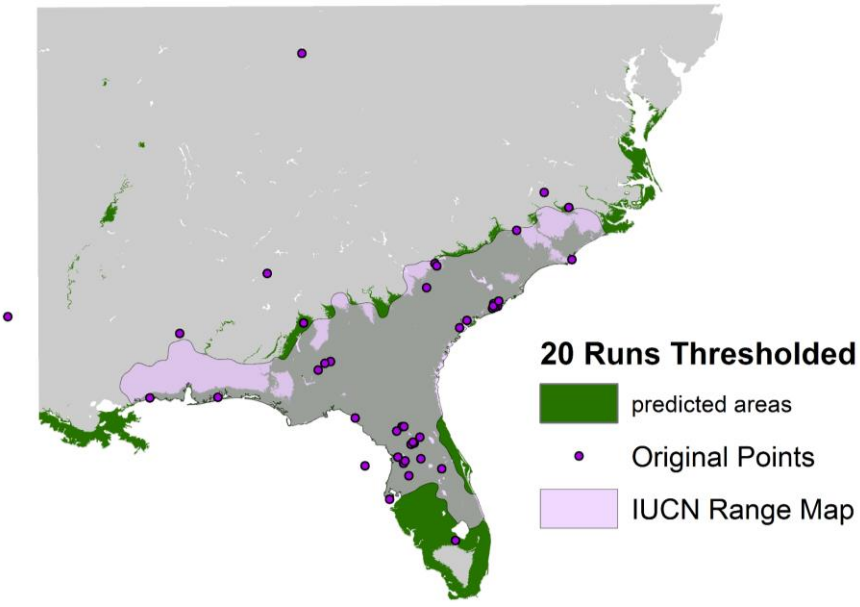

Convex Hull
Original Points
Background Points
Convex Hull

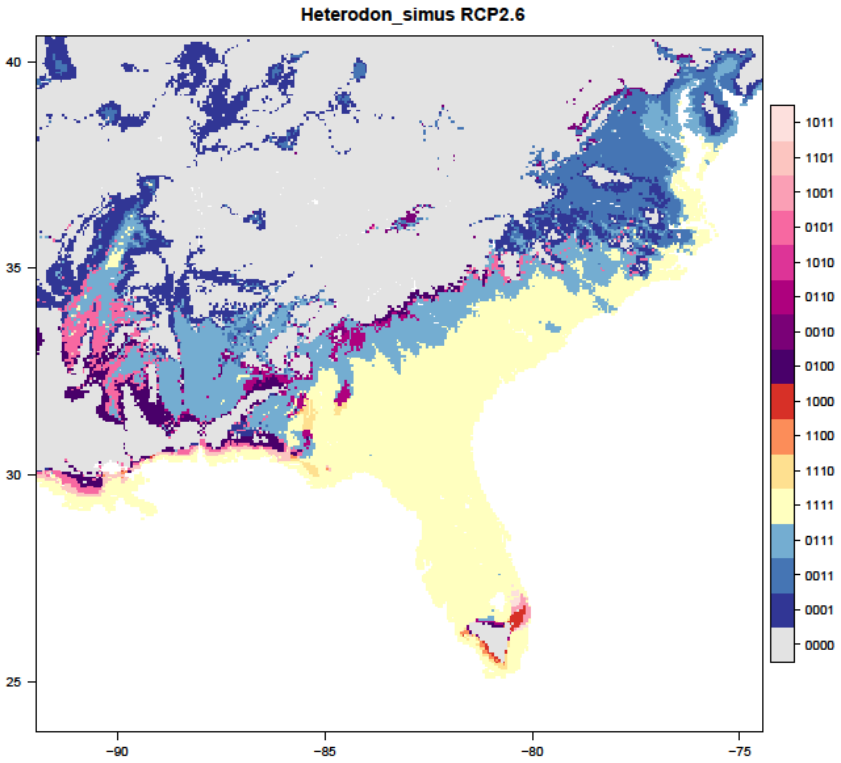

Subsampled Points
1 Run
1
0

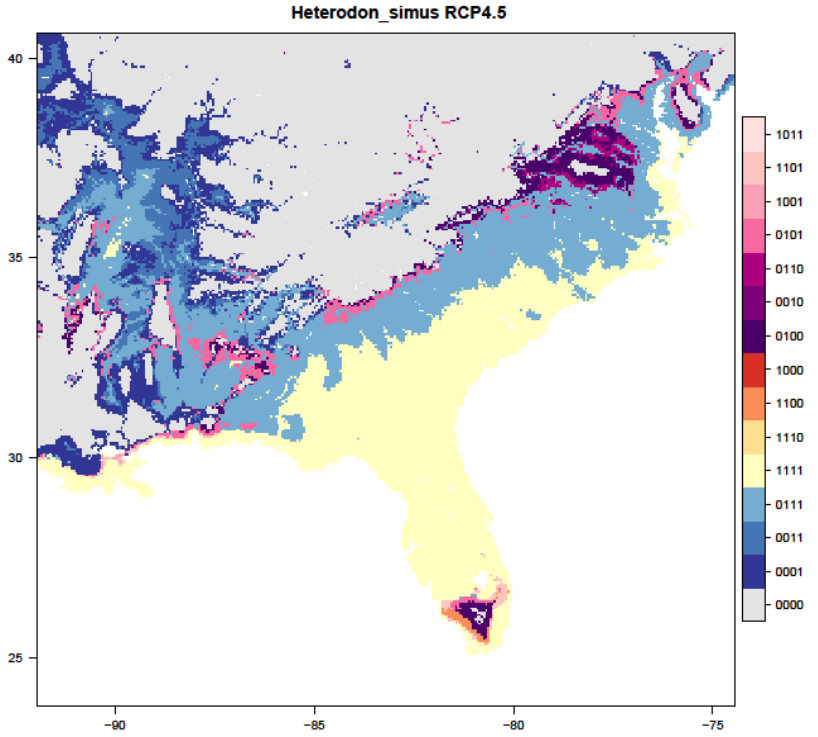

1 Run Thresholded
predicted range
Subsampled Points


Original Points
20 Runs
1
0


20 Runs Thresholded
predicted areas
Original Points


20 Runs Thresholded
predicted areas
Original Points
IUCN Range Map


Heterodon_simus RCP2.6
40
35
30
25
−90
−85
−80
−75
1011
1101
1001
0101
1010
0110
0010
0100
1000
1100
1110
1111
0111
0011
0001
0000


Heterodon_simus RCP4.5
40
35
30
25
−90
−85
−80
−75
1011
1101
1001
0101
0110
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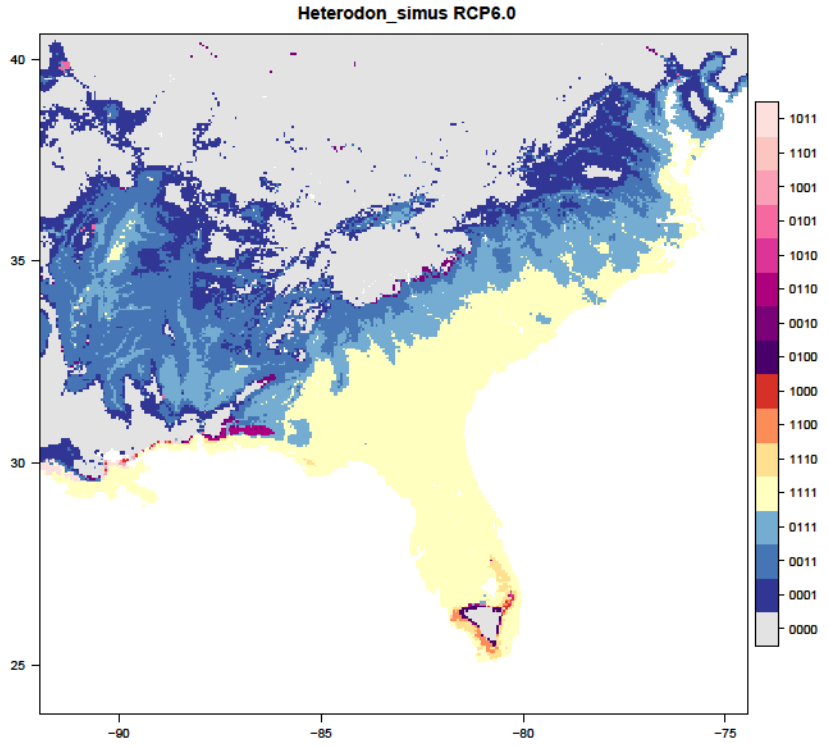
1111
0111
0011
0001
0000


Heterodon_simus RCP6.0
40
35
30
25
−90
−85
−80
−75
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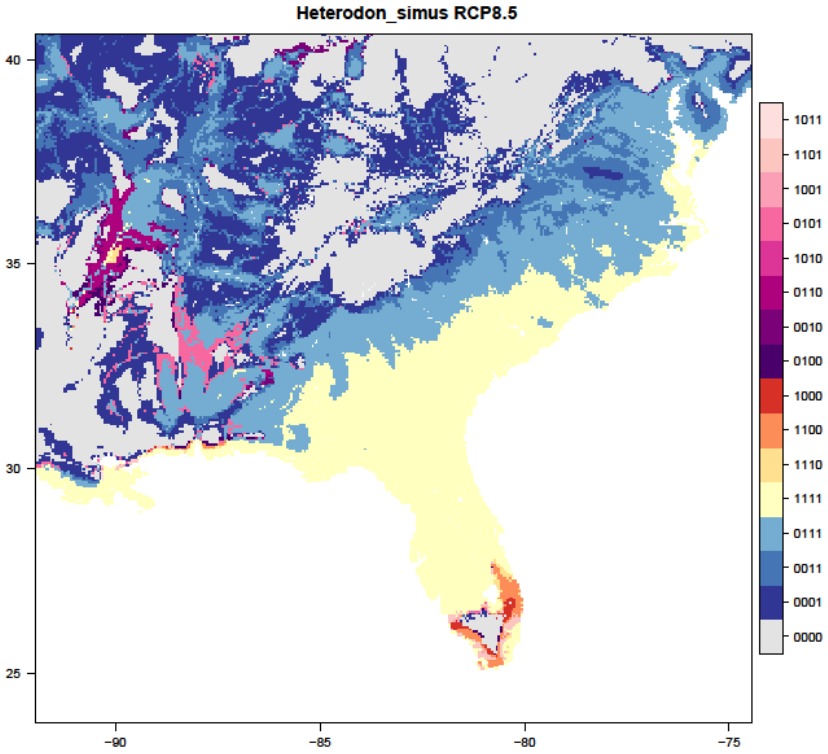
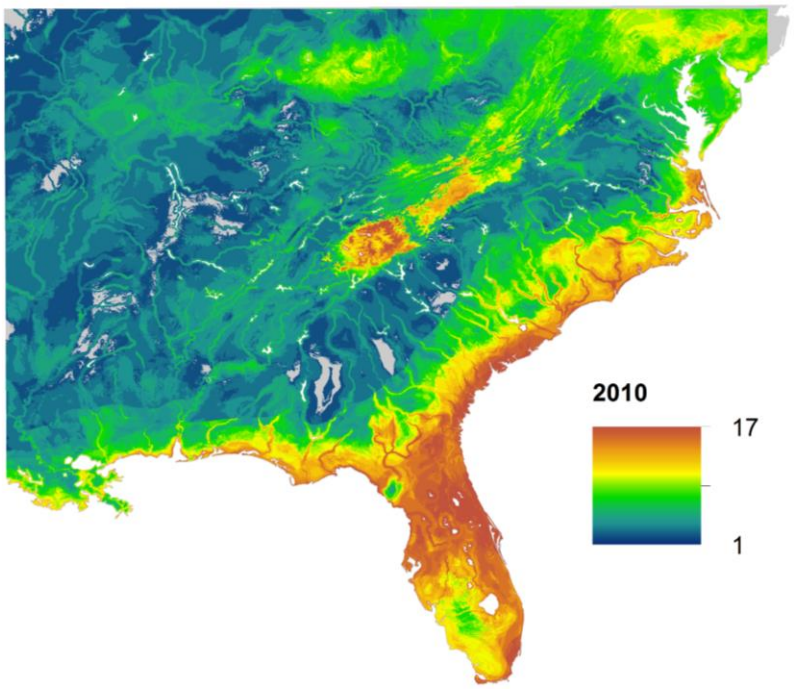
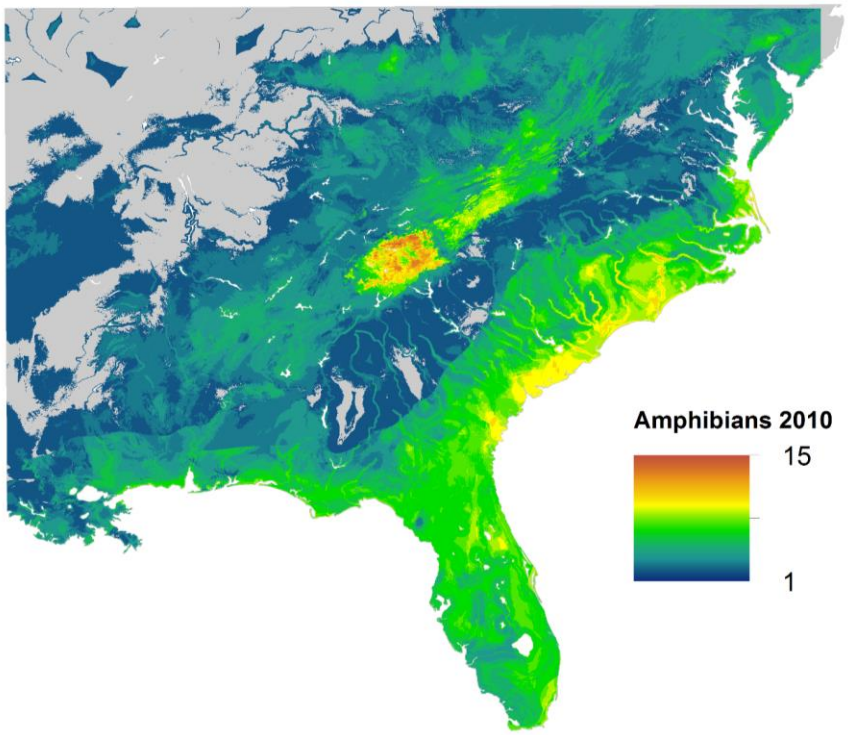

Heterodon_simus RCP8.5
40
35
30
25
−90
−85
−80
−75
1011
1101
1001
0101
1010
0110
0010
0100
1000
1100
1110
1111
0111
0011
0001
0000

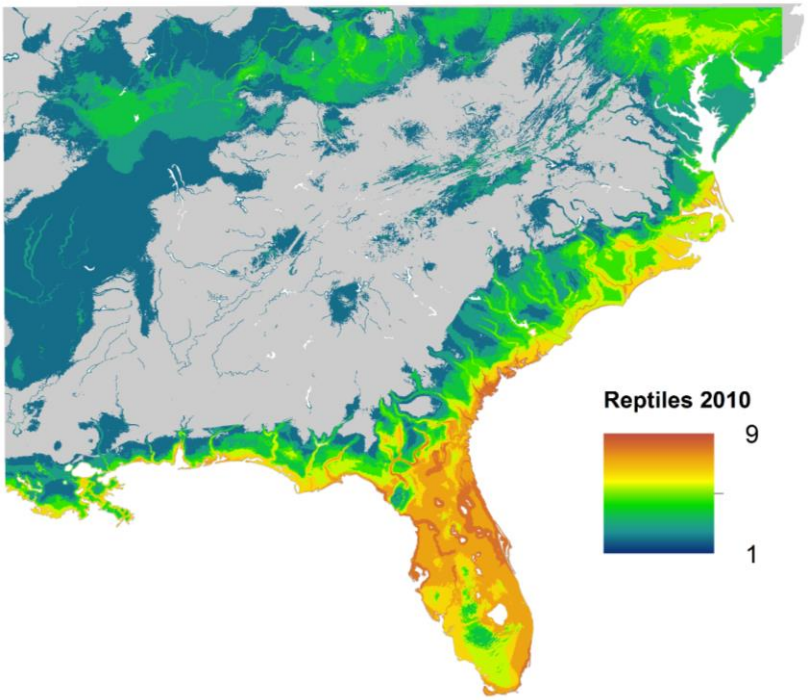
Projection	Number of Cells	Cell Change from 2010	Number Cells in Protected Land	Number of Cells in Urbanized Land	T1notT2	T2notT1	Overlap	Centroid X	Centroid Y
2010	421257	0	84543	305340	0	0	0	-82.33468826	31.01648015
RCP2.62030	761363	340106	110955	516770	6391	346497	414866	-83.67549466	32.17296023
RCP2.62050	804888	383631	112908	498107	15105	398736	406152	-82.31430251	33.07785737
RCP2.62070	1011461	590204	123805	617697	10496	600700	410761	-83.26584915	33.70864653
RCP4.52030	983727	562470	131705	659777	872	563342	420385	-82.73029968	33.14294371
RCP4.52050	958531	537274	121048	613986	12812	550086	408445	-83.5018154	33.33976216
RCP4.52070	1193280	772023	141384	740367	3909	775932	417348	-84.36944021	33.61963083
RCP6.02030	673165	251908	110816	441332	5747	257655	415510	-82.4590086	32.26141093
RCP6.02050	1022365	601108	125494	650581	4442	605550	416815	-83.84003795	33.02446051
RCP6.02070	1270605	849348	138965	779343	13736	863084	407521	-84.10339695	33.76545586
RCP8.52030	921455	500198	123932	624790	3828	504026	417429	-83.10882365	33.28827981
RCP8.52050	1166105	744848	133430	756163	20239	765087	401018	-83.29920009	34.38249657
RCP8.52070	1585350	1164093	164008	1028189	17312	1181405	403945	-84.13080119	34.9479531

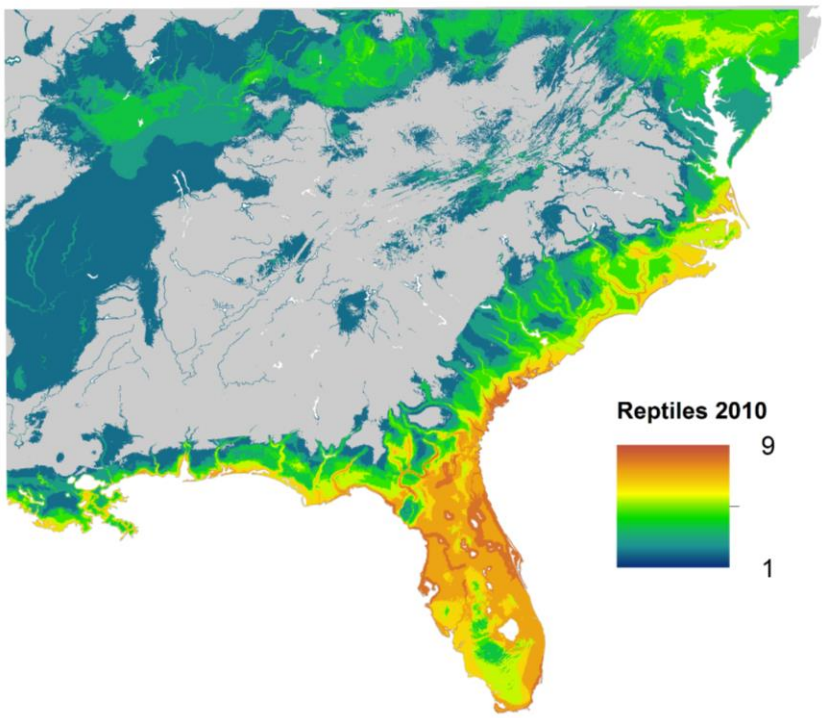
4.2 Overall Results

We also collected results that involved all of the species. The following maps are a sum of the number of species with a presence in that cell. This function produces biodiversity, or richness maps. These figures were made for all species, and also for all species in each class (amphibians, mammals, and reptiles).




Amphibians 2010
15
1


Reptiles 2010
9
1



These figures were created for every projection.

CHAPTER 5

DISCUSSION

Although we were happy with our results, these figures were not the ultimate goal of the project. We made these figures to begin to understand our data and our outputs, as it is difficult to individually observe thirteen projections for all of the species in our study. The information we wanted to gain from these results was:

1. How closely our models match with "official" ranges, like the published IUCN Red List ranges
2. The types of shifts we can expect to see in future work (contractions, growths, etc.)
3. What post-processing will need to be done on our results (smoothing algorithms, removing "outlier" habitat)
4. Which species are viable to use in future work (have habitats in all time periods, exhibit "interesting" movement)

Once we have finished running our experiments for all of our species, we will be better equipped to make these observations. During this study we did not spend much time looking at the outputs and the figures, except to confirm that the methodology produced accurate results for a few test species.

In general, we want the species distribution models for each species to use in future research. In our given time frame, we were not able to begin calculating the migration corridors. This is the next step in the project, but it could not be done without first collecting the data in this study.

Not only will we continue to use the data collected for the species in this study, the methodology that was developed and tested can be used in any research involving species distribution models and their projections. Because most of our time was spent developing and automating these methods, our R scripts and documentation might be the most important outcome of this project. Given environmental data and species occurrence points, the entire process can be easily replicated for any experiment.

CHAPTER 6

CONCLUSIONS

Species distribution models are constantly being used in the field of ecology, and although software such as Maxent exists to make the process much easier, there are still many decisions to be made in the methodology to increase model accuracy. Many of the steps are lengthy and repetitive if they need to be applied to many species. This is why it was important in our study to spend the time developing these methods and R scripts. It would be infeasible to collect the species distribution data for about 300 species in a reasonable timeframe without an "easy to use" workflow.

Using the R scripts also made it easier to test our methods and ensure that we were happy with every step in the process. For example, subsampling the occurrence points and generating our own background points were not added until very late in our study. However, we did not need to make any changes to our previous work to add this new step because it was simple to add these methods to the pipeline.

Although we were not able to finish getting results for all of our species, the experiments can now be run with minimal observation. If we decide to change the list of species or our chosen environmental rasters, it is easy to switch data in and out. We hope that our process will be helpful not only for our own future work, but also for others.

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